

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 10, 2005, 17:19:54 ; Search time 489.5 Seconds
(without alignments)
6145.500 Million cell updates/sec

Title: US-10-667-281-1
Perfect score: 7137
Sequence: 1 tgcctcaatgcagcgatctg.....ggaggtctgaggggtagc 3889

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/US10667281/runat 10092005 172901.11861/app query.fasta_1.4039
-DB=A Geneseq -QFWT=fastan -SUPPLX=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORES=ptc -THR MAX=100 -THR MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10667281 @CEN 1.1 570 @runat 10092005 172901.11861 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 16Dec04:.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5264	73.8	967	8	ADQ39940 Human myo
2	5264	73.8	967	8	ADQ39941 Human myo
3	5259	73.7	967	2	AAW80285 Human int
4	5251	73.6	967	8	AAY04142 Human Tan
5	5251	73.6	967	8	ADRI4133 Human NF-
6	5248	73.5	968	4	AAW50011 Protein;
7	5228	73.3	967	2	AAW78189 Human sec
8	5228	73.3	967	6	ADAS7139 Human sec
9	5228	73.3	967	6	ADA41003 Human sec
10	5228	73.3	967	7	ADB91631 Human sec

11	5228	73.3	967	7	ADC74267	Adc74267 Human sec
12	5228	73.3	967	7	ADD37948	Add37948 Human sec
13	5183	72.6	949	7	ADG72483	Adg72483 Human agg
14	5179	72.6	950	8	ADO20218	Ado20218 Human PRO
15	5179	72.6	950	8	ADQ39942	Adq39942 Human myo
16	5174	72.5	950	4	AAW49501	Aaw49501 Human MET
17	5174	72.5	950	4	AAW73549	Aaw73549 Human ADA
18	5174	72.5	950	4	AAW50002	Aaw50002 Human MET
19	4326.5	60.6	988	6	ABU08387	Abu08387 Murine ma
20	4247.5	59.5	950	3	AAW53899	Aaw53899 Amino aci
21	4019.5	56.3	896	3	AAW21265	Aaw21265 Mouse met
22	3940	55.2	727	2	AAW78435	Aaw78435 Human ADA
23	2504.5	35.1	924	5	ABP70062	Abp70062 Human NOV
24	2486.5	34.8	950	5	AAE22541	Aae22541 Human pro
25	2486.5	34.8	950	6	ABU09520	Abu09520 Human pro
26	2486.5	34.8	950	6	ADQ88214	Adq88214 Human 655
27	2482.5	34.8	950	6	ABR40092	AbR40092 Human ADA
28	2480.5	34.8	950	4	AAW62299	Aaw62299 Human met
29	2464.5	34.5	952	5	AAU74751	Aau74751 Human pro
30	2417	33.9	928	5	AAU72899	Aau72899 Human met
31	2335.5	32.7	890	6	ABP96306	Abp96306 Human ADA
32	2333.5	32.7	890	8	ADK70513	Adk70513 Respirato
33	2332.5	32.7	890	2	AAW49502	Aay49502 Human MET
34	2332.5	32.7	890	4	AAW50003	Aab50003 Human MET
35	2325	32.6	889	4	AAW74946	Aab74946 Human ADA
36	2274.5	31.9	905	4	AAW72284	Aab72284 Murine AD
37	2199	30.8	823	6	ABU08383	Abu08383 Human mat
38	2136	29.9	837	4	AAW78228	Aag78228 Human agg
39	2136	29.9	837	7	ADB85488	Adb85488 Human agg
40	2136	29.9	840	3	AAW21256	Aab21256 Human met
41	2131	29.9	837	2	AAW75425	Aaw75425 Human agg
42	2131	29.9	837	7	ADJ69542	Adj69542 Human hea
43	2131	29.9	837	8	ADS20209	Ads20209 Human agg
44	2128	29.8	846	8	ADS20232	Ads20232 Human agg
45	2124	29.8	837	3	AAW99429	Aay99429 Human PRO

ALIGNMENTS

RESULT 1

ADQ39940

ID ADQ39940 standard; protein; 967 AA.

XX AC ADQ39940;

XX XX

XX DT 18-NOV-2004 (first entry)

XX XX Human myocardial infarction-associated gene derived protein, SEQ ID 1603.

XX DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX XX cardiant; gene therapy; human.

XX KW Homo sapiens.

XX OS

XX XX WO2004058052-A2.

XX XX

XX PD 15-JUL-2004.

XX XX

XX PF 22-DEC-2003; 2003WO-US040978.

XX XX

XX PR 20-DEC-2002; 2002US-0434778P.

XX PR 10-MAR-2003; 2003US-0453135P.

XX PR 30-APR-2003; 2003US-0466412P.

XX PR 23-SEP-2003; 2003US-0504955P.

XX PR (APPL-) APPLERA CORP.

XX PA Cargill M, Devlin JJ, Iakubova O;

XX PI WPI; 2004-533949/51.

XX DR N-PSDB; ADQ39112.

XX XX Identifying an individual who has an altered risk for developing

XX PT

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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 10, 2005, 19:13:05 ; Search time 495.5 Seconds
(without alignments)
6191.500 Million cell updates/sec

Title: US-10-667-281-1
Perfect score: 7137
Sequence: 1 tgcctcaatgcagcgatctg.....ggaggctgtgaggggtacg 3889

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 3554922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DBV=xlp
-O=/cgn2_1/USPTO.spool.p/US10667281/runat_10092005_172904_11961/app.query.fasta_1.4039
-DB=Published Applications AA -QFMT=fasta -SUFFIX=top25.rapb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10667281.OCGN 1 1 563 @runat_10092005_172904_11961
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp:
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp:
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp:
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp:
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp:
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp:
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp:
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp:
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp:
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp:
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp:
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp:
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pcp:
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pcp:
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pcp:
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp:
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp:
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5264	73.8	967	17	US-10-741-600-1603	Sequence 1603, Ap
2	5264	73.8	967	17	US-10-741-600-1604	Sequence 1604, Ap
3	5264	73.8	967	18	US-10-923-035-37	Sequence 37, Appl
4	5284	73.8	967	18	US-10-756-149-5619	Sequence 2, Appl
5	5259	73.7	967	13	US-10-105-929-2	Sequence 2, Appl
6	5259	73.7	967	14	US-10-115-286-2	Sequence 2, Appl
7	5259	73.7	967	16	US-10-757-450-2	Sequence 2, Appl
8	5251	73.6	967	16	US-10-755-889-134	Sequence 134, App
9	5248.5	73.5	968	10	US-09-373-658-135	Sequence 125, App
10	5230	73.3	967	11	US-09-989-687-126	Sequence 126, App
11	5183	72.6	949	17	US-10-667-281-2	Sequence 2, Appl
12	5179	72.6	950	17	US-10-741-600-1605	Sequence 1605, Ap
13	5179	72.6	950	18	US-10-973-858-14	Sequence 14, Appl
14	5174	72.5	950	10	US-09-373-658-2	Sequence 2, Appl
15	5174	72.5	950	11	US-09-989-687-2	Sequence 2, Appl
16	5079	71.2	931	9	US-09-741-151-4	Sequence 4, Appl
17	4326.5	60.6	968	13	US-10-163-316-7	Sequence 7, Appl
18	4326.5	60.6	968	16	US-10-391-364-82	Sequence 82, Appl
19	4296.5	60.2	951	15	US-10-381-793-3	Sequence 3, Appl
20	4292.5	60.1	950	9	US-09-321-9878-4	Sequence 1, Appl
21	3940	55.2	727	9	US-09-445-023A-1	Sequence 1, Appl
22	3940	55.2	727	14	US-10-097-597-1	Sequence 1, Appl
23	3940	55.2	727	14	US-10-097-580-1	Sequence 1, Appl
24	3674	51.5	727	9	US-09-445-023A-12	Sequence 12, Appl
25	3674	51.5	727	14	US-10-097-597-12	Sequence 12, Appl
26	3674	51.5	727	14	US-10-097-580-12	Sequence 12, Appl
27	3321	46.5	608	9	US-09-803-589-2	Sequence 2, Appl
28	3321	46.5	608	16	US-10-718-332-2	Sequence 2, Appl
29	3315	46.4	608	9	US-09-803-589-8	Sequence 8, Appl
30	3315	46.4	608	13	US-10-105-929-13	Sequence 13, Appl
31	3315	46.4	608	16	US-10-718-332-8	Sequence 8, Appl
32	2874	40.3	577	15	US-10-425-114-39241	Sequence 39241, A
33	2812	39.4	551	9	US-09-802-582-16	Sequence 16, Appl
34	2812	39.4	551	13	US-10-105-929-16	Sequence 16, Appl
35	2812	39.4	551	14	US-10-365-227-16	Sequence 16, Appl
36	2649	37.1	518	9	US-09-803-589-10	Sequence 10, Appl
37	2649	37.1	518	16	US-10-718-332-10	Sequence 10, Appl
38	2504.5	35.1	924	15	US-10-093-463-28	Sequence 28, Appl
39	2487	34.8	978	15	US-10-275-107-59	Sequence 59, Appl
40	2486.5	34.8	950	9	US-09-741-151-2	Sequence 2, Appl
41	2486.5	34.8	950	9	US-09-965-631-4	Sequence 4, Appl
42	2486.5	34.8	950	16	US-10-391-364-77	Sequence 77, Appl
43	2486.5	34.8	950	17	US-10-753-267-56	Sequence 56, Appl
44	2486.5	34.8	950	17	US-10-961-020-4	Sequence 4, Appl
45	2480.5	34.8	950	16	US-10-763-210-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-741-600-1603
; Sequence 1603, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1603
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1603

Alignment Scores:

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OM nucleic - protein search, using frame_plus_n2p_model

Run on: September 10, 2005, 18:10:55 ; Search time 124.5 Seconds
(without alignments)
6011.036 Million cell updates/sec

Title: US-10-667-281-1
Perfect score: 7137
Sequence: 1 tgcctcaatgcagcgatctg.....ggaggctgctgaggggtagc 3889

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USPTO.spool.p/US10667281/runat 10092005 172902 11880/app query.fasta_1.4039
-DB=PIR -QFMT=fastan -SUFFIX=top25.rpr -MINMATCH=0.1 -LOPECT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667281 @CGN 1 1 194 @runat 10092005 172902 11880 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4296.5	60.2	951	2 T00017	Gene ADAMTS-1 prot
2	3074	43.1	550	2 T47158	hypothetical prote
3	2136	29.9	837	2 T00355	hypothetical prote
4	1613	22.6	2165	2 T21371	hypothetical prote
5	1120.5	15.7	1205	2 T18517	procollagen N-endo
6	651	9.1	1558	2 C89114	protein C3/C3.6a
7	651	9.1	2167	2 T34395	hypothetical prote
8	649.5	9.1	1444	2 T18856	angiogenesis inhib
9	475	6.7	860	2 T16892	hypothetical prote
10	435.5	6.1	1059	2 T22545	hypothetical prote
11	411	5.8	957	2 T15976	hypothetical prote
12	405	5.7	951	2 T00260	hypothetical prote
13	381.5	5.3	903	2 S60257	metrin alpha - mo
14	345.5	4.8	549	2 S48169	metalloproteinase

15	342	4.8	617	2	S48160	metalloproteinase
16	339	4.7	571	2	S24789	jarathagin C precu
17	338	4.7	826	2	A60385	monocyte surface a
18	334.5	4.7	609	2	S55270	catrocollastatin p
19	334	4.7	610	2	JC8056	halyase - Gloydin
20	328	4.6	655	2	JC7850	disintegrin and me
21	322	4.5	610	2	JC7530	vascular apoptosis
22	317.5	4.4	481	2	JC4342	fibrinolytic prote
23	307.5	4.3	481	2	S43125	truncin precursor
24	305.5	4.3	478	2	A43296	atrolysin B (EC 3.
25	305	4.3	616	2	A55796	ecarin precursor -
26	303.5	4.3	407	2	S66260	metalloproteinase
27	303.5	4.3	478	2	JQ1301	hemorrhagic protei
28	303	4.2	411	1	HYSNFA	fibrinase (EC 3.4.
29	300	4.2	814	2	G02390	disintegrin-like m
30	295.5	4.1	478	2	JC4880	fibrinolytic metal
31	289.5	4.1	480	1	A30065	trigamin precursor
32	282.5	4.0	484	2	JC8020	metalloproteinase
33	282	4.0	789	2	S28259	androgen-regulated
34	282	4.0	1572	2	T00027	brain-specific ang
35	276.5	3.9	1074	2	JC5928	semaphorin F precu
36	272.5	3.8	508	2	T22836	hypothetical prote
37	271.5	3.8	414	1	HYRSAC	atrolysin C (EC 3.
38	270	3.8	660	2	S71949	metalloproteinase
39	269	3.8	414	2	S41609	atrolysin C (EC 3.
40	266.5	3.7	1170	2	A40558	thrombospondin 1 p
41	264	3.7	952	2	T18900	disintegrin and me
42	263	3.7	776	2	S28258	androgen-regulated
43	261	3.7	670	2	I65967	disintegrin-like m
44	260.5	3.6	419	2	S41607	atrolysin A (EC 3.
45	258.5	3.6	905	2	S55059	fertilin alpha-I -

ALIGNMENTS

RESULT 1

T00017

Gene ADAMTS-1 protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Mar-2004

C:Accession: T00017

R:Kuno, K.; Lizasa, H.; Ohno, S.; Matsushima, K.

Genomics 46, 466-471, 1997

A:Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 ge

A:Reference number: Z14055; MUID:98110583; PMID:9441751

A:Accession: T00017

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-951 <KUN>

A:Cross-references: EMBL:AB001735; NID:g2809056; PIDN:BAA24501.1; PID:g2809057

A:Experimental source: strain 129SVJ

C:Genetics:

A:Gene: ADAMTS-1

A:Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2

F:542-598/Domain: thrombospondin type 1 repeat homology <THR3>

Alignment Scores:

Pred. No.:	6,77e-261	Length:	951
Score:	4296.50	Matches:	789
Percent Similarity:	88.10%	Conservative:	55
Best Local Similarity:	82.36%	Mismatches:	99
Query Match:	60.20%	Indels:	15
DB:	2	Gaps:	5

US-10-667-281-1 (1-3889) x T00017 (1-951)

QY	59	ATGGGGAACGGAGAGCGGGCTCCGGGGTCTCGAGGCTTTGGGCCCGTACCACGCTGCTG 118
Db	1	MetGlyApValGlnArgAlaArgSerArgGlySerLeuSerAlaHisMetLeu 20
QY	119	CTGCTCGCGCGCGCG-----CTACTGCGCGTGTGCGAGCACTCGGGCGCCCTCC 169
Db	21	LeuLeuAlaSerIleThrMetLeuLeuCysAlaArgGlyAlaHisGlyArgProthr 40

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 10, 2005, 17:23:24 ; Search time 620.5 Seconds
(without alignments)
6418.939 Million cell updates/sec

Title: US-10-667-281-1
Perfect score: 7137
Sequence: 1 tgcctcaatgcagcgatctg.....ggaggctgtcgagggttagc 3889

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DRV=xlp
-O=/cgn2.1/USPTO spool_p/US10667281/runat_10092005 172901 11868/app query.fasta_1.4039
-DB=UniProt -QPWT=fastan -SUPFIX=top25.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*
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2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5259	73.7	967	1 ATSI HUMAN	Q9uh18 homo sapien
2	5251	73.6	967	2 Q8NE26	Q8ne26 homo sapien
3	4326.5	60.6	968	1 ATSI MOUSE	P97857 mus musculus
4	4325	60.6	967	2 Q6BEJ2	Q6bej2 rattus norv
5	4319	60.5	967	1 ATSI RAT	Q9wuc1 rattus norv
6	3921.5	54.9	759	2 Q8HZM8	Q8hzm8 equus caball
7	2486.5	34.8	950	1 AT15 HUMAN	Q8tes8 homo sapien
8	2332.5	32.7	890	1 AT58 HUMAN	P9719 homo sapien
9	2274.5	31.9	905	1 AT58 MOUSE	P57110 mus musculus
10	2131	29.9	837	1 AT54 HUMAN	Q75173 homo sapien
11	2124	29.8	837	2 Q6UWA8	Q6uwa8 homo sapien
12	2113	29.6	837	2 Q6P4O8	Q6p4o8 homo sapien
13	2111	29.6	833	2 Q8K384	Q8k384 mus musculus
14	2110.5	29.6	845	2 Q8BNJ2	Q8bnj2 mus musculus
15	2083	29.2	839	2 Q7YS95	Q7ys95 bos taurus
16	1991.5	27.9	893	2 Q6A017	Q6a017 mus musculus

17	1981	27.8	630	1 AT54 RAT	Q9esp7 rattus norv
18	1923	26.9	930	1 AT55 HUMAN	Q9una0 homo sapien
19	1913	26.8	930	1 AT55 MOUSE	Q9u01 mus musculus
20	1906	26.7	928	2 Q6TY19	Q6ty19 rattus norv
21	1871	26.2	1306	1 AT20 MOUSE	P59511 mus musculus
22	1845.5	25.9	1935	1 AT59 HUMAN	Q9p2n4 homo sapien
23	1808.5	25.3	867	2 Q66KM3	Q66km3 xenopus tro
24	1749	24.5	1911	1 AT20 HUMAN	P59510 homo sapien
25	1678	23.5	623	2 Q8BGF4	Q8bpf4 m mus muscu
26	1617	22.7	562	1 AT15 MOUSE	P59384 mus musculus
27	1613	22.6	2165	2 Q19791	Q19791 caenorhabdi
28	1362	19.1	1841	2 Q68SA9	Q68sa9 mus musculus
29	1325	18.6	1686	2 Q6P7J9	Q6p7j9 homo sapien
30	1324	18.6	1221	2 Q6P4R5	Q6p4r5 homo sapien
31	1317.5	18.5	1081	1 AT18 HUMAN	Q8te60 homo sapien
32	1304	18.3	1077	1 AT10 HUMAN	Q9h324 homo sapien
33	1299	18.2	1224	1 AT16 HUMAN	Q8tes7 homo sapien
34	1289	18.1	1593	1 AT12 HUMAN	P58397 homo sapien
35	1284.5	18.0	1070	2 Q8CG28	Q8cg28 mus musculus
36	1283	18.0	1233	2 Q69Z28	Q69z28 mus musculus
37	1279.5	17.9	1009	2 Q8BKY1	Q8bky1 m mus muscu
38	1279.5	17.9	1600	2 Q811B3	Q811b3 mus musculus
39	1274.5	17.9	1059	2 Q9W493	Q9w493 drosophila
40	1265.5	17.7	1537	2 Q7KSH7	Q7ksh7 drosophila
41	1265.5	17.7	1688	2 Q8SXB0	Q8sxb0 drosophila
42	1215.5	17.0	997	1 AT57 HUMAN	Q9ukp4 homo sapien
43	1207.5	16.9	988	2 Q7PW77	Q7pwy7 anopheles g
44	1201	16.8	1092	2 Q8BKA1	Q8bka1 mus musculus
45	1162	16.3	900	2 Q8K206	Q8k206 mus musculus

ALIGNMENTS

RESULT 1
ATSI_HUMAN
ID ATSI_HUMAN STANDARD; PRT; 967 AA.
AC Q9UH18; Q9NSJ8; Q9P2K0; Q9UH83; Q9UP80;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-1 precursor (SC 3.4.24.-) (A disintegrin and metalloproteinase
with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).
GN Name=ADAMTS1; Synonyms=K1A1346, METH1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Casas C., Pritchard M.A., Estivill X., Arbones M.L.;
RT "Cloning, characterization and mapping on human chromosome 21 of the
orthologue of murine Adamts-1.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=Heart;
RX MEDLINE=99367466; PubMed=10438512; DOI=10.1074/jbc.274.33.23349;
RA Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,
RA Lombardo M., Iruela-Arispe M.L.;
RT "METH-1, a human orthologue of ADAMTS-1, and METH-2 are members of a new
family of proteins with angio-inhibitory activity.";
RN [3]
RP J. Biol. Chem. 274:23349-23357(1999).
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=20247184; PubMed=10785405;
RA Glienke J., Schmitt A.O., Pillarsky C., Hinzmann B., Weiss B.,
RA Rosenthal A., Thierach K.H.;
RT "Differential gene expression by endothelial cells in distinct
angiogenic states.";
RL Eur. J. Biochem. 267:2820-2830(2000).
RN [4]
RP SEQUENCE FROM N.A.

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 10, 2005, 18:17:56 ; Search time 100 Seconds
(without alignments)
5806.204 Million cell updates/sec

Title: US-10-667-281-1
Perfect score: 7137
Sequence: 1 tgcctcaatgcagcgtatcg.....ggaggtctgtgaggggtatgc 3889

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued Patents AA -QPMT=fastan -SUFFIX=cp25.ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=25
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5259	73.7	967	4	US-09-130-491-2
2	5183	72.6	949	4	US-09-568-559-2
3	4292.5	60.1	950	4	US-09-321-987B-4
4	3940	55.2	727	4	US-09-445-023A-1
5	3674	51.5	727	4	US-09-445-023A-12
6	3315	46.4	608	4	US-09-130-491-13
7	2812	39.4	551	4	US-09-130-491-16
8	2480.5	34.8	950	3	US-10-009-332-1
9	2274.5	31.9	905	3	US-09-369-364A-9
10	2131	29.9	837	4	US-09-122-126B-2
11	2131	29.9	837	4	US-09-634-286A-2
12	2131	29.9	837	4	US-10-247-685-2

13	1923	26.9	930	4	US-09-122-126B-15	Sequence 15, Appl
14	1923	26.9	930	4	US-09-634-286A-15	Sequence 15, Appl
15	1923	26.9	930	4	US-10-247-685-15	Sequence 15, Appl
16	1911	26.8	930	3	US-09-369-364A-2	Sequence 2, Appl
17	1736.5	24.3	1882	3	US-09-369-364A-13	Sequence 13, Appl
18	1623.5	22.7	2150	4	US-09-321-987B-2	Sequence 2, Appl
19	1620.5	22.7	874	3	US-09-369-364A-15	Sequence 15, Appl
20	1613	22.6	2165	4	US-09-800-729-155	Sequence 155, App
21	1393.5	19.5	481	4	US-09-130-491-8	Sequence 8, Appl
22	1318	18.5	1104	4	US-09-981-953A-4	Sequence 4, Appl
23	1300	18.2	1224	4	US-09-930-872-4	Sequence 4, Appl
24	1300	18.2	1224	4	US-10-217-774-4	Sequence 22, Appl
25	1299	18.2	518	3	US-09-369-364A-22	Sequence 2, Appl
26	1213.5	17.0	908	4	US-09-963-791-2	Sequence 7, Appl
27	1205.5	16.9	997	3	US-09-369-364A-7	Sequence 17, Appl
28	1201.5	16.8	1081	3	US-09-369-364A-17	Sequence 24, Appl
29	1152.5	16.1	757	4	US-09-963-791-24	Sequence 11401, A
30	1128.5	15.8	1211	4	US-09-949-016-11401	Sequence 5, Appl
31	1120.5	15.7	969	4	US-09-321-987B-5	Sequence 5, Appl
32	1111.5	15.6	1211	4	US-09-491-522-5	Sequence 11, Appl
33	1088.5	15.3	1205	4	US-09-491-522-11	Sequence 5, Appl
34	1032	14.5	770	4	US-09-981-953A-2	Sequence 11, Appl
35	1027.5	14.4	859	3	US-09-369-364A-5	Sequence 7859, Ap
36	1015	14.2	1039	4	US-09-949-016-7859	Sequence 12, Appl
37	780	10.9	589	4	US-09-963-791-12	Sequence 22, Appl
38	719	10.1	438	4	US-09-963-791-22	Sequence 11, Appl
39	716.5	10.0	245	3	US-09-369-364A-11	Sequence 89, Appl
40	601	8.4	1745	4	US-09-800-729-89	Sequence 10, Appl
41	592.5	8.3	507	4	US-09-963-791-10	Sequence 21, Appl
42	574.5	8.0	525	3	US-09-369-364A-21	Sequence 8, Appl
43	571.5	8.0	724	4	US-09-784-358-8	Sequence 12, Appl
44	571.5	8.0	845	4	US-09-784-358-12	Sequence 2, Appl
45	571.5	8.0	1691	4	US-09-784-358-2	

ALIGNMENTS

RESULT 1
US-09-130-491-2
; Sequence 2, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-491-2

Alignment Scores:
Pred. No.: 0
Score: 5259.00
Percent Similarity: 99.79%
Best Local Similarity: 99.69%
Query Match: 73.69%
DB: 4
Length: 967
Matches: 964
Conservative: 1
Mismatches: 2
Indels: 0
Gaps: 0

US-10-667-281-1 (1-3889) x US-09-130-491-2 (1-967)

QY 8 ATGCAGCATCTGTGCCGAGGGTTTCGGAAGCGCAAGCTGGCGGACATGGGGNAC 67
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